

STIC Search Report Biotech-Chem Library

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TO: Cynthia Wilder

Location: REM/2A35/2C18

Wednesday, April 20, 2005

Art Unit: 1637

Case Serial Number: 09/529397

From: David Schreiber

Location: Biotech-Chem Library

Remsen E01A61

Phone: 571-272-2526

David.Schreiber@uspto.gov

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ALIGNMENTS

BP.

ant tumour; signal transmission regulation; ifferentiation; aptamer; inflammation; ss. Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation. g Ras target protein. (NISC-) JAPAN SCI & TECHNOLOGY CORP. Sakamoto K; 98JP-00242596. 98JP-00333284. 99WO-JP004399. Yokoyama S, Hirao I, WPI; 2000-224330/19. 13-AUG-1999; 14-AUG-1998; 24-NOV-1998; 24-FEB-2000.

m) 24 /98

Claim 6; Page 41; 59pp; Japanese.

The invention relates to novel nucleic acids which bind specifically to the target protein of Ras, e.g. Raf-1. RNA aptamer (AAZ99024-Z99051) based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras target protein and regulating transmission of signal

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Gaps ; 0

Indels

Length 100;

Score 100; DB 12; Pred. No. 2.7e-25;

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sequence is a synthetic RNA 9A aptamer (100-mer) given in an exemplification of the invention.
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                                                       Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;
                                                                                                                                                                                                                                   61 AUUGGUUUUNAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 100
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(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic RNA 9A(5Iy87) aptamer (100-mer).
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                                                                                                         Local Similarity
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                                                                                                                                                                Gaps
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                                                                         Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.
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                                   Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;
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 causing proliferation or differentiation of cells
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(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                      100.0%; Score 100; DB 3;
100.0%; Pred. No. 2.7e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yokoyama S, Hirao M, Mitsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                          ADJ10063 standard; DNA; 100 BP
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ADJ10063
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Location/Qualifiers

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This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(1H)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkrynl or amino group, blotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as
                                                                                                                                                                                                                         Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating
Hirao M, Mitsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 10; 78pp; Japanese.
                                                                                                                  WPI; 2004-122944/12.
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the nucleosides

nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, ribozymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide

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nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, ribozymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA 94 (51987) aptamer (100-mer) given in an exemplification of the invention.
   of the
   which is applied as template for the integration of
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Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;

9 9 1 GGGAGUGGAGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCAAACCAGUUAUAA Gaps ö 100.0%; Score 100; DB 12; Length 100; 100.0%; Pred. No. 2.7e-25; ive 0; Mismatches 0; Indels 0 Local Similarity 100. es 100; Conservative Query Match Best Loca Matches g

61 AUUGGUUUUNAGCAUAUGCCUUAGCGACAGCUUCUGC 100

61 AUGGUUUAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 100

RESULT 4 ADJ10065

ADJ10065 standard; DNA; 200

(first entry) 17-JUN-2004

Synthetic RNA 2x9A aptamer (200-mer)

ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.

Synthetic.

WO2004007713-A1

22-JAN-2004

28-FEB-2003; 2003WO-JP002342

17-JUL-2002; 2002JP-00208568

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. (RIKE) RIKEN KK. (NISC-) JAPAN SCI & TECHNOLOGY CORP

Hirao M, Mitsui Hirao I, Yokoyama S,

WPI; 2004-122944/12.

Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating

Disclosure; Fig 10; 78pp; Japanese

This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(1H)-pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription

ö with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as base which is applied as template for the integration of any of the uncleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, ribozymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids acids are cemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA 2x9A aptamer (200-mer) given in an 9 Gaps malignant tumour; signal transmission regulation cell differentiation; aptamer; inflammation; ss. ö Length 200; Indels Sequence 200 BP; 50 A; 44 C; 48 G; 0 T; 58 U; 0 Other; 61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCAGCUUCUGC 100 Autocituturaccatatucccituaccaccaccaccaccitica 100 Score 100; DB 12; Pred. No. 3.4e-25; RNA aptamer #27 for binding Ras target protein. Mismatches Sakamoto K; exemplification of the invention. ; 0 SCI & TECHNOLOGY 100.0%; 99WO-JP004399 98JP-00242596 98JP-00333284 AAZ99050 standard; RNA; 90 (first entry) Matches 100; Conservative Yokoyama S, Hirao I, Ras target protein; cell proliferation; WPI; 2000-224330/19 Similarity W02000009684-A1 (NISC-) JAPAN Homo Sabiens. 13-AUG-1999; 14-AUG-1998; 24-NOV-1998; 21-JUN-2000 24-PEB-2000. AAZ99050; Query Match Local RESULT 5 AAZ99050 8 \times 9 \times 9 g ð 엄

The invention relates to novel nucleic acids which bind specifically to the target protein of Ras, e.g. Raf-1. RNA aptamer (AAZ99024 299051) based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras target protein and regulating transmission of signal causing proliferation or differentiation of cells Nucleic acid e.g. RNA aptamer capable of binding specifically to trarget protein like Raf-1, useful in drug compositions to treat an diagnose malignant tumors and inflammation. Claim 6; Page 42; 59pp; Japanese.

Sequence 90 BP; 23 A; 19 C; 22 G; 0 T; 26 U; 0 Other;

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        90.06;
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Best Local Similarity 100.
Matches 90; Conservative
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17-JUN-2004 (first entry) ADJ10053 standard; RNA; ADJ10053;

ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.

RNA aptamer (RNA9A) SeqID 1

Unidentified

402004 007713-A1 22-JAN-2004 28-FEB-2003; 2003WO-JP002342.

17-JUL-2002; 2002JP-00208568.

(RIKE) RIKEN KK. (NISC-) JAPAN SCI & TECHNOLOGY CORP. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

ij Hirao M, Mitsui Hirao I, Yokoyama S,

WPI; 2004-122944/12

Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating diseases

Example 4; SEQ ID NO 1; 78pp; Japanese.

unitural base, namely the 5-substituted.2-oxo(1H)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, fetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids of containing a 6-substituted-2-aminopurin-9-yl group as base which is applied as template for the integration of any of the nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, riboxymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, creplication and transcription for their preparation. This polynucleotide sequence is an RNA aptamer (RNA9A) given in an exemplification of the This invention relates to nucleosides or nucleotides that a novel invention.

Sequence 98 BP; 24 A; 21 C; 24 G; 0 T; 29 U; 0 Other;

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                                                                  1 GGGAGUGGAGGAAUUC--UGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUAUAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignant tumour; signal transmission regulation; cell differentiation; aptamer; inflammation; ss.
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                                                                                                       61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCAUCUGC 100
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                                                                                                                                 98
                                                                                                                      59 AUUGGUUUTAGCAUAUGCCUVAGCGACAGCAAGCUUCUGC
Score 84.4; DB 12;
Pred. No. 8.9e-20;
                                                                                                                                                                                                                                                                          RNA aptamer #28 for binding Ras target protein.
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                                                                                                                                                                                                                                                                                                     Ras target protein;
                                                                                                                                                                                                                                                                                                                cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-224330/19.
             Similarity
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                                                                                                                                                                                                                                                                                                                                                                     WO200009684-A1.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1998;
24-NOV-1998;
                                                                                                                                                                                                                                                   21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yokoyama S,
                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Query Match
             Best_Local
Matches 9
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RESULT 9 AAZ99076

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Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating
                                                                                 ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.
                                                                                                                                                                                                                    (RIKE ) RIKEN KK.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                          Hirao M, Mitsui T;
                                                                  Synthetic RNA 0C aptamer (100-mer).
                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 10; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the invention
         ADJ10066 standard; DNA; 147 BP.
                                                                                                                                                                                28-FEB-2003; 2003WO-JP002342.
                                                                                                                                                                                                   17-JUL-2002; 2002JP-00208568
                                              (first entry)
                                                                                                                                                                                                                                                          Yokoyama S,
                                                                                                                                                                                                                                                                            WPI; 2004-122944/12.
                                                                                                                                          WO2004007713-A1
                                               17-JUN-2004
                                                                                                                                                              22-JAN-2004
                                                                                                                         Synthetic
                            ADJ10066;
                                                                                                                                                                                                                                                          Hirao I,
                                                                                                                                                                                                                                                                                                                            diseases.
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unatural base, namely the 5'-substituted-2-oxo(1H)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive crowin a base substituted at the 5-position with either a photoreactive crowin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyhlocrescein, tetramethyl-7-carboxyhhodamine or caids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as the mucleotides into its complementary position. Accordingly, the nucleosides into its complementary position. Accordingly, the nucleosides are useful in developing functional nucleic acids are useful in developing functional nucleic acids containing a containing 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA OC aptamer (100-mer) given in an
This invention relates to nucleosides or nucleotides that a novel
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GGGAGUGGAGGAAUUCGAUCGAGGAACCCUAUCUGGUUUGGUAGCUGUAUU 60
                                                                                               Gaps
                                                                 1;
                                DB 12; Length 147;
                                          ,,
9e-08;
~hes 24; Indels
                                                                                                                                                                60 AAUUGGUUUUVAGCAUAUGCCUUVAGCGACAGCAAGCUUCUGC 100
                                                                                                                                                                                   61 CACCUGUAACAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 101
Sequence 147 BP; 32 A; 34 C; 37 G; 0 T; 44 U; 0 Other;
                                                                 0; Mismatches
                              Score 50.6;
Pred. No. 9e
                                50.6%;
                                                               76; Conservative
                                                 Best Local Similarity
                                                                 Matches
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8 a 8

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

Human ORFX ORF668 polynucleotide sequence SEQ ID NO:1335

(first entry)

08-FEB-2001

AAC75113;

BP

AAC75113 standard; cDNA; 748

RESULT 10 AAC75113/

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tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel nucleic acids which bind specifically to the target protein of Ras, e.g. Raf-1. RNA sequences (AAZ99076-Z99077) represent the sequence of aptamer inserts that bind the Ras target protein which are used to generate PCR primers. Aptamers based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras
                                                                                                                               protein; malignant tumour; signal transmission regulation; feration; cell differentiation; aptamer; inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                               Ras target protein-RNA binding sequence #1 for generating primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target protein and regulating transmission of signal causing proliferation or differentiation of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.0%; Score 45; DB 3; Length 45; 100.0%; Pred. No. 5.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AUGUCGACUCCGUCUUCCAUCAAACCAGUUAUAAAUUGGUUUUAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AUGUCGACUCCGUCGUCCUUCAAACCAGUUAUAAAUUGGUUUUAG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45 BP; 11 A; 10 C; 7 G; 0 T; 17 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 52; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                     Sakamoto K;
AAZ99076 standard; RNA; 45 BP
                                                                                                                                                                                                                                                                                                                                   98JP-00333284.
                                                                                                                                                                                                                                                                                    99WO-JP004399.
                                                                                                                                                                                                                                                                                                                   98JP-00242596.
                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     Hirao I,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-224330/19.
                                                                                                                                   Ras target protein;
cell proliferation;
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                                                                                                                                                                                                            16200009684-A
                                                                                                                                                                                                                                                                                                                   14-AUG-1998;
24-NOV-1998;
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                                                                 21-JUN-2000
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                                                                                                                                                                                                                                                   24-FEB-2000
                                AAZ99076;
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RESULT 11

us-09-529-397c-25.rng

immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antibacterial; antifungal; antihemmatic; antithytoid; antival; antibacterial; antifungal; antihemmatic; antithytoid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythemacosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; Claim 5; Page 1146-1147; 5507pp; English 99US-0127607P. 99US-0127636P. 99US-0127728P. thrombosis; contraceptive; ss 31-MAR-2000; 2000WO-US008621 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763. Shimkets RA, Leach M; (CURA-) CURAGEN CORP. WPI; 2000-602362/57. P-PSDB; AAB40904 WO200058473-A2 Homo sapiens 31-MAR-1999; 02-APR-1999; 05-OCT-2000

Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

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antipsoriatic; antiparkine sum as organization described to settly antiparkine sum as organization in the settly of antipsoriatic; antiparkine sum as organization anticonvulsant; antiarthritic; immunosuppressant; immunosimulant; cardiant; thrombolytic; coagulant; vancinosist antibacterial; dermatological; immunosuppressive; antitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral; bacterial or fungal infection, malaria, autoimmune cationare, asthman, allergies, aplastic ansemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

Sequence 748 BP; 134 A; 218 C; 221 G; 174 T; 0 U; 1 Other;

TEGGGTCGACCTCGACGCTTCTTCAGACCGTTGATGAAAGGGTTGTAGGTCATG 258 18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG 77 Gaps 0; Score 30.6; DB 3; Length 748; Pred. No. 1.7; 29; Indels 12; Mismatches 30.6%; 46.8%; 36; Conservative Local Similarity 317 Query Match Matches

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cccredecacedeaadc 241 94 CCUUAGCGACAGCAAGC 78

Human, open reading frame, ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; Human ORFX polynucleotide sequence SEQ ID NO:17493. ABN24508 standard; cDNA; 748 BP. 2000US-0206132P. 2000US-0228716P. 29-MAY-2001; 2001WO-US010836. myasthenia gravis; gene; ss. (first entry) WO200192523-A2 Homo sapiens. 30-MAY-2000; 29-AUG-2000; 24 - JUN - 2002 06-DEC-2001 ABN24508; ABN24508/

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Shimkets RA, Leach MD; (CURA-) CURAGEN CORP.

2002-106308/14.

P-PSDB; ABP08756.

Disclosure; SEQ ID NO 17493; 1037pp; English.

Treferred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX creating or proventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide syndrome associated with ORFX-associated disorder. ORFX polymucleotide treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders related to organ transplantation, cardiovascular diseases, disorders melated to organ transplantation, cardiovascular diseases, disorders, infectious circage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thilammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, repercusion injury in various tissues and conditions resulting from repencent of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/published_pct_sequences The present invention describes substantially purified human proteins

Sequence 748 BP; 134 A; 218 C; 221 G; 174 T; 0 U; 1 Other;

30.6%; Score 30.6; DB 6; Length 748; 46.8%; Pred. No. 1.7; Best Local Similarity Query Match

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Propionibacterium acnes immunogenic polypoptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and cancerage of the care is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and determining P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and dispostic agents for determining P. acnes presence, for example, by carywe linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAUS7347-AAUS7508 and AAUG7590-AAUG7591. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pct_sequences
                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthealnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                     18 UCGAGGCAUAUGUCGACUCCGUCUUCCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein encoding DNA #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhatia A;
  Indels
  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang SS,
, Jen S, Carter D;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 78; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW, Persing DH, Mitcham J
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                AASS9583 standard; DNA; 15776 BP
  12;
                                                                                                                                                           257 cccredecacedadec 241
                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000US-0199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2000; 2000US-0208841P.
                                                                                                                        CCUUAGCGACAGCAAGC
                                                                                                                                                                                                                                                                                                                                              13-FEB-2002 (first entry)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2001.
  36;
                                                                                                                     78
                                                                                                                                                                                                                                                                                                      AAS59583;
  Matches
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The invention relates to an isolated polynucleotide (ACF64415-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymentionic fusion proteins comprising a polypeptide of the invention; an exhod for stimulating an immune response specific for a P. acnes to hypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, or polymeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for determining the presence of P. acnes in a catient; and a method for inhibiting the development of P. acnes in a patient; The P. acnes polypeptides, polymericides, antigen-presenting cells that express the polypeptides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne polypeptides are useful for diagnosing, preventing or treating acnes proteins, The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                              11
                                                                                                                              18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUVAGCAUAUG
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maisonneuve JL;
Jones R, Carter D;
Sequence 15776 BP; 3393 A; 4931 C; 4483 G; 2969 T; 0 U; 0 Other;
                                        30.6%; Score 30.6; DB 4; Length 15776; 46.8%; Pred. No. 4.5; ive 12; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW, Persing DH, Bhatia A,
ng S, Jen S, Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes DNA contig sequence #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 78; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                   ACF64512 standard; DNA; 15776 BP.
                                                                                                                                                                                                                                                           8487 CCCTGGGCACGGAAGC 8503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                   78 CCUUAGCGACAGCAAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                        Query Match
Best Local Similarity 46.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                             ACF64512;
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AAZ99049;
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                                                                                                                                                                                                                                                                                                 New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                    sequence represents a P. acnes DNA contig which is specifically claimed in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The A. baumanni nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for
                                                                                                                                                                                                                                                                        18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                      Sequence 15776 BP; 3393 A; 4931 C; 4483 G; 2969 T; 0 U; 0 Other;
                                                                                                                                                                                                                            .,
                                                                                                                                                                                Length 15776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 366;
                                                                                                                                                                                                                              Indels
and the kit is useful for performing a diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 366 BP; 131 A; 65 C; 63 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding Acinetobacter baumannii protein #608.
                                                                                                                                                                                                                            29;
                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 30.4%; Score 30.4; DB 9; Similarity 39.8%; Pred. No. 1.7; 35; Conservative 17; Mismatches 36;
                                                                                                                                                                                                       4.5;
                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                30.6%; Score 30.6;
46.8%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 608; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; plant biocontrol agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00328352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA29321 standard; DNA; 366
                                                                                                                                                                                                                                                                                                                                                              CCUUAGCGACAGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                            CCCTGGGCACGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                            36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ADA33447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6562958-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                          8487
                                                                                                                                                                                                                                                                                                                                                           78
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                                                                                                                                                                                                                                                                                                                  8427
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
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                                                                                                                                                                                                                            Matches
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AC ADA2
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101 GGGTGTTTATGAATATAGCTTTCTATATGTCGCACCAGTAATTGTGCAAAGAAGTAATAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignant tumour; signal transmission regulation; cell differentiation; aptamer; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 30; DB 3; Length 98; 63.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98 BP; 24 A; 24 C; 26 G; 0 T; 24 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA aptamer #26 for binding Ras target protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                               TCTGGTTTATGCGTATATTCTAGATTCA 14
                                                             61 AUUGGUUUUAGCAUAUGCCUUAGCGACA
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Job time : 432 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 41; 59pp; Japanese.
                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP004399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-00242596,
98JP-00333284,
                                                                                                                                                                                                                                                                      AAZ99049 standard; RNA; 98
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirao I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ras target protein;
cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-224330/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tokoyama S,
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Sequence 324280, Sequence 324280, Sequence 324280, Sequence 790, App Sequence 130987, Sequence 150280, Sequence 14431, A

US-10-322-281-744
US-10-479-081-104
US-10-097-111-10
US-10-097-111-10
US-10-097-111-10
US-10-271-181B-6
US-10-271-181B-6
US-10-27-632-199104
US-10-027-632-199104
US-10-027-632-199104
US-10-027-632-199104
US-10-027-632-324280
US-10-027-632-34433
US-10-027-632-101724
US-10-027-632-101724
US-10-027-632-101724
US-10-027-632-101724
US-10-027-632-101724
US-10-027-632-101724
US-10-027-632-32481

Sequence 35948, A Sequence 85, Appl Sequence 199104,

Sequence Sequence Sequence

522 56506 1116 1884 48995

Sequence 15351, A Sequence 324279,

Sequence

Sequence 162, App Sequence 162, App Sequence 310, App Sequence 73812, A Sequence 73810, A Sequence 73810, A

US-10-329-624-162 US-10-425-115-310 US-10-437-963-73812 US-10-470-048B-23 US-10-437-963-73810 US-10-437-963-73813

ALIGNMENTS

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Gaps

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Length 4285; Indels

DB 14;

29.8%; Score 29.8; D 33.3%; Pred. No. 11; tive 22; Mismatches

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67

Sequence 14431, A Sequence 14432, A Sequence 101724, Sequence 101724, Sequence 13160, A Sequence 1680, Ap Sequence 24541, Ap

368 725 725 740 740 740 740 720 7286 8998

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Sequence 1, Application US/10104580
Sequence 1, Application US/10104580
Publication No. US20030033628A1
GENERAL INFORMATION:
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in TITLE OF INVENTION: poplar and other plant species.
TITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 6486
CURRENT PILING DATE: 2002-03-21
FRIOR FILING DATE: 1999-10-01
FRIOR FILING DATE: 1999-10-01
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1998-04-06
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; ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNAGCAUAUGCCUUAGCGACA 88
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LENGTH: 4285
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US-10-104-580-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Appli
Sequence 1, Appli
Sequence 25760, A
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Sequence 40631, A
                                                                                                                                                        April 19, 2005, 13:28:09 ; Search time 5352 Seconds (without alignments) 113.354 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                   1 gggaguggaggaauucaucg......uagcgacaagcaucugc 100
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| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBFW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBFW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
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//ptodata/2/pubpna/US07_PUBCOMB.seq:*
                        version 5.1.6
- 2005 Compugen Ltd.
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10S-09-38-842A-2908

10S-09-938-842A-2908

10S-09-938-842A-2908

7 US-10-425-114-30801

8 US-10-357-930-24310

8 US-10-77-701-13576

8 US-10-425-115-121623
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US-10-419-723-1
US-10-369-493-25760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                     5622541 seqs, 3033355566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                     GenCore
Copyright (c) 1993
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18
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17
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Maximum DB seq length: 2000000000
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586
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Match
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                                                                                                               OM nucleic -
                                                                                                                                                                                                                                                                                                       Sequence:
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US-09-938-842A-2908
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/2020
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/203,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                             Sequence 40631, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2908, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION: APPLICANT: Harper, Jeff
TYPE: DNA
ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                        RESULT 2
US-10-282-122A-40631/C
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GATT 500
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US-09-938-842A-2908/c
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: WANG, Xun
APPLICANT: WANG, Xun
APPLICANT: WANG, Xun
APPLICANT: Thu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
FRIOR APPLICATION NUMBER: US 60/227,866
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2908
LING DATE: 2000
LINGS BENCE FILING DATE: 2000-06-22
SEQ ID NO 2908
FRIOR FILING DATE: 2001-06-22
SEQ ID NO 2908
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.6%; Score 28.6; DB 9; Length 2000; Best Local Similarity 35.8%; Pred. No. 21; Matches 24; Conservative 19; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2908
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ORGANISM: Arabidopsis thaliana
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699 GTTTTTA 693
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699 GTTTTTA 693
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3
; COHER INFORMATION: n = A,T,C or G
US-10-357-930-24310
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ORGANISM: Zea mays
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                                       Sequence 30801, Application US/10425114

Publication No. US20040034888A1

Sequence 30801, Application US/10425114

SEQUENCEMT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 30801

LENGTH: 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GGGGCATTTTTATGTTGTTATAGATTCTCTCCTGCTCCACCGCCATCATAAACTCGGTT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: UC-ZMFLB73080F09_FLI
US-10-425-114-30801
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24310, Application US/10357930 Publication No. US20040259086A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Zea mays FEATURE:
                                  US-10-425-114-30801/c
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Sequence 121623, Application US/10425115
| Publication No. US20040214272A1
| Publication No. US20040214272A1
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwei
| APPLICANT: Chou, Yihua APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: NumBER 0216322)B |
| CURRENT APPLICATION NUMBER: 2003-04-28 |
| CURRENT PILING DATE: 2003-04-28 |
| SEQ ID NO 121623 |
| LENGTH: 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other Molecules Associated With
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                                                                                                                      Sequence 13576, Application US/10767701

Sequence 13576, Application US/10767701

Publication No. US2040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yindwa

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(51535)8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 13576

LENGTH: 1612
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Length 1161;
                                                              Indels
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US-10-767-701-13576
      DB 18;
                                                              18; Mismatches 38;
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Query Match 28.2%; Score 28.2; E
Best Local Similarity 37.1%; Pred. No. 24;
Matches 33; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                        818 GTTTAACTTATGCCTTAAAGAATTAAAGC 790
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Best Local Similarity 38.2%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Sorghum bicolor
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us-09-529-397c-25.rnpb

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-419-723-1
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                                                                                              Length 1851;
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                                                                                                                                               Indels
                                                                                         Query Match 28.2%; Score 28.2; DB 18; Best Local Similarity 37.1%; Pred. No. 29; Matches 33; Conservative 18; Mismatches 38;
                      , OTHER INFORMATION: Clone ID: MRT4577_42398C.1 US-10-425-115-121623
                                                                                                                                                                                                                                                                                                                   1273 CCAGCAAGCGCATTAGGGAAAGGAAGATT 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10067514
Publication No. US20030054531A1
GENERAL INFORMATION:
APPLICANT: Gretarsdottir, Solveig
APPLICANT: Jonsdottir, Sif
APPLICANT: APPLICANT: Reynisdottir, Sif
ITILE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 99/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                          68 UUAGCAUAUGCCUUAGCGACAGCUU 96
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1691139
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: ELEMESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                           127542 AGTTGATCCATGCTTTTTGGAGGGAGCTTATCCCTTCAAAGGGAATAAAAAGTGTTTTAG 127483
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  Length 1691139;
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 748
28.0%; Score 28; DB 17; Length 16
41.7%; Pred. No. 4e+02;
tive 15; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.8%; Score 27.8; D
Best Local Similarity 38.0%; Pred. No. 33;
Matches 27; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                      US-10-369-493-25760

. Sequence 25760, Application US/10369493

. Publication No. US20030233675A1

. GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 744, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
  Query Match
Best Local Similarity 41.7*
Matches 25; Conservative
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SEQ ID NO 25760
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CORGANISM: Homo sapiens
US-10-322-281-744
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GENERAL INFORMATION:
APPLICANT: PELETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: GROS, PHILLIPPE
: APPLICANT: GROS, PHILLIPPE
: APPLICANT: GROSDE, PHILLIPPE
: TITLE OF INVENTION: ENCODE ANTI-MICROBIAL POLYPEPTIDES
: TITLE OF INVENTION: ENCODE ANTI-MICROBIAL POLYPEPTIDES
: TITLE OF INVENTION NUMBER: US/10/097,111
: CURRENT APPLICATION NUMBER: 09/676,412
: PRIOR APPLICATION NUMBER: 09/676,412
: PRIOR PLING DATE: 1000-09-29
: PRIOR FILING DATE: 1099-09-30
: NUMBER OF SEQ ID NOS: 552
: SOFTWARE: PATENTI VET. 2.1
: SEQ ID NO 47
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40.0%; Pred. No. 47;
tive 15; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                         Query Match 27.6%; Score 27.6; DB 19; Best Local Similarity 47.6%; Pred. No. 33; Matches 39; Conservative 9; Mismatches 34;
                                    FEATURE:
NAME/KBY: misc feature
LOCATION: (711).
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
LOCATION: (732).. (732)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 47, Application US/10097111; Publication No. US20030138771A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10, Application US/10097111; Publication No. US20030138771A1; GENERAL INFORMATION:
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                                                                                                                                                                                                              ; OTHER INFORMATION: nbla-03439-f
US-10-479-081-104
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246 AATGCAGTTGACAC 260
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Best Local Similarity 40.0%
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  LOCATION: (706)..(706)
OTHER INFORMATION: n is a,
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US-10-097-111-10
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Sequence 104, Application US/10479081
; Sequence 104, Application US/10479081
; Publication No. US20050059001A1
; GENERAL INFORMATION:
    APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: WUCLEIC ACIDS ISOLATED FROM NEUROBLASTOMA
; FILE REFERENCE: 7388-80893
; CURRENT APPLICATION WUMBER: US/10/479,081
; CURRENT FILING DATE: 2003-11-26
; PRIOR PAPLICATION NUMBER: PCT/JP02/05295
; PRIOR FILING DATE: 2002-05-30
; PRIOR PAPLICATION NUMBER: JP 2001-163666
; PRIOR PELING DATE: 2001-06-31
; PRIOR PELING DATE: 2001-06-31
; RIOR APPLICATION NUMBER: JP 2001-155260
; PRIOR FILING DATE: 2001-06-24
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE PATENTIN VETSION 3.2
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OTHER INFORMATION: n is a,
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THER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (73)...(73)
OTHER INFORMATION: n is a,
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LOCATION: (87)...(87)
OTHER INFORMATION: n is a,
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LOCATION: (90)...(90)
OTHER INFORMATION: n is a,
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LOCATION: (566)..(566)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LENGTH: 732
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| TITLE OF INVENTION: DNA SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE EPI THAT
| TITLE OF INVENTION: ENCODE ANTI-MICROBIAL POLYPEPTIDES
| FILE REPERENCE: 073406-06.063
| CURRENT APPLICATION NUMBER: US/10/097,111
| PRIOR APPLICATION NUMBER: 09/676,412
| PRIOR APPLICATION NUMBER: 00/157,218
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Search completed: April 19, 2005, 15:28:25 Job time : 5357 secs

BQ531573 APEX2_5 F BQ531573 APEX2_5 F BQ531501 APEX3_35 CF791691 880034 MA BG649176 EM1_77_E0 BE363373 WS1_62_B0

CH240_325 Bn01b_03j BW594105 BW545837

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Mus muscu

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Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

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Searched:

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Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM2-HT0224-291
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stop: 415.
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1 (bases 1 to 642)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
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Homo sapiens
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AUTHORS
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                                                                                                                   April 19, 2005, 13:28:09 ; Search time 3095 Seconds (without alignments) 1229.863 Million cell updates/sec
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AG069018
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- 2005 Compugen Ltd.
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Listing first 45 summaries
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ABG31824
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                                                                                                                                                                                                                             AZ955882
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KEYWORDS
                                                                                                                                                                                                                                                                                                                    ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jb, Wit.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Phone: 81-298-36-9189, fax: 81-298-36-9199
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG557770 149 bp DNA linear GSS 05-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-476B14.T7, genomic survey
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                  12 AAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCAAACCAGUUAUAAAUUGGUUUUAG 71
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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Direct Submission
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                                                                                                                                                        34.6%; Score 34.6; DB 2; Length 642; 37.0%; Pred. No. 0.71; tive 22; Mismatches 29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'tissue type="mixture of kidney and spleen"
'clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/gub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:57486"
/clone="MSMg01-476B14.T7"
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                                                                                                                                                                                                                                                                                                                                                                   210 AATTTGCGTTTACAACAACAA 230
                                                                                                                                                                                                                                                                                                                                     72 CAUAUGCCUUAGCGACAGCAA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e-mail: abe@rtc.riken.jp
PRIMERS
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AG557770.1 GI:48318468
GSS.
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Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 749)
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Best Local Similarity 51.09
Matches 25; Conservative
                                                                                                                                                                                                      30; Conservative
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LIBRARY
                                                                                                                                                                                 Best Local Similarity
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R.Site 2
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                                                                                                                                                            Query Match
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AG557770/c
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                                                                                                                                                                                                      Matches
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TITLE
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectiek kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAPA2 (gil-#A7321141gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xill0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                             AZ955882
2M0222110F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0222110 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
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31.2%; Score 31.2; DB 8; Length 442; 32.6%; Pred. No. 9.8; ive 24; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: I column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="UUGC2M0222110"
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                       AZ955882.1 GI:13827109
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Best Local Similarity 32.6%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Rattus norvegicus (Norway rat)
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Matches 29, Conserve
                                                                                       Rattus.
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AMGNNUC:MRBE4-00015-C9-A rat brain E15 (10375) Rattus norvegicus
cDNA clone mrbe4-00015-c9 5', mRNA sequence.
CB736914.1 GI:29804127
                                                                                                                                                                                     B21536 696 bp DNA linear GSS 16-SEP-1997 F21F23-T7 IGF Arabidopsis thaliana genomic clone F21F23, genomic
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                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 696)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
                   272 GCAGGCTTTCATCCCAGCATCTGATTCCTGAGTCTTCATTGATAAAATCTAACAATTGAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCAAACCAGUUAUAAAUUGGUUU 68
 /sex="hermaphrodite"
/clone_lib="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dept. of Biology, University of Pennsylvania, Philadelphia, PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
                                                                                     332 TTTTTGTTTTTGTTTTCGAGACCAGGTTTCT 363
                                                                   67 UUUAGCAUAUGCCUUAGCGACAGCAUCU 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jecker@atgenome.bio.upenn.edu
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Produced by Thomas Altmann"
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University of Pennsylvania
                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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High quality sequence stop: 143.
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/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               BAC End Sequences at ATGC
Unpublished (1997)
Other_GSSs: F21F23-Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="F21F23"
                                                                                                                                                                                                                         Burvey sequence.
B21536
B21536.1 GI:2396590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rel: 215-898-9384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          969. .1
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CB736914/c
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1074 bp mRNA linear EST 21-JUL-2000 6121621621F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586661 5', BE371824
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8748 row: j column: 06

High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="mxbe4-00015-c9"
/tissue_type="brain B15"
/clone_lib="rat brain B15 (10375)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: Not1; rat
brain B15"
                                                                                                                                                                                   Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Incompanded (2007)
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.6%; Score 30.6; DB 6; Length 461; 36.7%; Pred. No. 16; ive 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                              Tel: 805 447-4881
Plate: 00015 row: c column: 9.
Location/Qualifiers
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Mus musculus
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120 TGAGCAGTTGCATTAGCAA 102
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                                                                                                        1 (bases 1 to 461)
Amgen EST Program.
Amgen Rat EST Program
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22 GGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCUU 81
                                                                                                                                                                                                                                                      5', mRNA sequence.
CK016754
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503 TAAGTAGTAG 594
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                                                                                                                   306 CCCG 303
                                                                            82 AGCG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Matanabe,H. and Sakaki,Y.

Totoki,Y., Matanabe,H. and Sakaki,Y.

Direct Submission

Submitted (12-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gscriken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                             /clone lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidarectionally. PrimeF: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG069018 917 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-059H17.R, genomic survey sequence.
                                                                                                                                                                                                                                                                                             78
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                /tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab host="DH10B"
                                                                                                                                                                                                                                                      Gaps .
                                                                                                                                                                                                                                                                                             19 CGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGC
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-059H17.R"
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39.1%; Pred. No. 20;
tive 18; Mismatches
/clone="IMAGE:3586661"
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

Cyprinidomes; Cyprinidae; Danio.

1 (Dases 1 to 725)

S NIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

CDNA Library Preparation: Open Biosystems

CONA Library Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="NIH ZGC 10"
/note="Vector: pExpress1; Site_1: Not1; Site_2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. Ist strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CK016754 11near EST 26-NOV-2003
AGENCOURT_16544280 NIH_ZGC_10 Danio rerio CDNA clone IMAGE:7043617
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366 GGTATCTGTCGCCCCCCCCCCCCCCACGCTGGGGTTATAAATGGATTTTAAATTATAAATTATAAATTGTCGTTACCCTT 307
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/db_xref="taxon:7955"
/clone="IMAGE:7043617"
/tissue_type="whole body"
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/organism="Danio rerio"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gore eudicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                             Library was constructed by Corina Guder / GATC Konstanz, Germany Library materials provided by Thomas Holstein / Molecular Cell Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu) Seq primer: -40UP High quality sequence stop: 565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. (bases 1 to 617)
Singh,J.A., Robert,L.S., Lu,B., Zhu,L., De Moors,A., Couroux,P.,
Harris,L.J., Hattori,J.I., Ouellet,T., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Singh,J.A.
Eastern Ceral and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R. WashU Hydra EST Project Whyblished (2002)
Other ESTs: taeA6908.x1
Contact: Hans Bode
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                                                                                                                                                               WashU Hydra EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre), Tl Phage resistant electrocompetent cells"
/lone lib="Hydra EST Darmstadt I"
/note="Wyetcor: pBluescript II SK (+); Site_1: Not1; Site_2: EcoRI"
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/strain="sf-1 mutant of strain 105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hydra magnipapillata"
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393 CAACGAGATCAAGTTT 378
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Glycine max
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Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                     Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Unter GSSB: CIT-HSP-2374K6.TR
CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS53623 578 bp mRNA linear EST 03-MAY-2004 tae26g08.yl Hydra EST Darmstadt I Hydra magnipapillata CDNA 5' similar to TR:Q9VJZ2 Q9VJZ2 CG6565 PROTEIN. ;, mRNA sequence.
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                                                      GSS 29-AUG-1998
                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (basea I to 528)
Adame, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
Hydridae; Hydra.
I toases I to 578)
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13.21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                              CIT-HSP-2374K6.TF CIT-HSP Homo sapiens genomic clone 2374K6
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2374K6"
                                                      528 bp
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Hydra magnipapillata
                                                                                                                                                                                            Homo sapiens (human)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         Venter, J.C.
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"I (bases 1 to 717)

Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,

Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,

Mattine,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,

Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,

Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,

Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.

Unpublished (2002)

Contact: Hans Bode
                                                                                                                                                                                                                                                                                                                       377 AGGGATATGGGCCACTTTGTGACCCAATGAACAAGTTGTGAACTAGTTTCATCATTTGAGT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: 1915. Control wostl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer.
Location/Qualifiers
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
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resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                                                                                                                                                                        626;
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/strain="sf-1 mutant of strain 105"
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/lab_host="TransforMax EC100
                                                                                                                                                                      ch 29.6%; Score 29.6; D
I Similarity 40.8%; Pred. No. 36;
31; Conservative 16; Mismatches
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40.8%; Pred. No. 37;
tive 16; Mismatches
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437 CAACAAGATCAAGTTT 452
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Fax: 314 286 1810
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/clone_lib="Gm01_AAFC_ECORC_Glycine_max_cold_stressed_leav
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Bode, H. Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, B., Bennett, J., Ronko, I., Tasqareishvili, R.,
Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                             /note="Vector: Bluescript SK-/Xhol-EcoRI; Site 1: EcoRI; Site 2: Xhol; Plants were grown 12 days from seeds, treated at 20C for 3 days, then leaves were collected. Library was prepared using Unizap ZAP-cDNA synthesis kit / Packaged Gigapack III Gold."
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Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer
High quality sequence stop: 626.
Location/Qualifiers
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Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 UUCAUCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCA
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/lab_host="TransforMax EC100 (Epicentre), Tl Phage
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
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/strain="sf-1 mutant of strain 105"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 29.6%; Score 29.6; D
1 Similarity 42.4%; Pred. No. 36;
36; Conservative 14; Mismatches
                                                                                         /organism="Glycine max"/mol_type="mRNA"
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                                                                                                                                                                   /db_xref="taxon:3847"
/clone="Gm01_01e04"
/tissue_type="Leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 UAUGCCUUAGCGACAGCAUCU 98
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                                           Location/Qualifiers
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WashU Hydra EST Project
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                                                                                                                                                                                                                                                                                                                                          Lundeberg, J.

EST analysis of brain and testis cDNA libraries from White leghorn and Red Jungle Fowl

Lundublished (2004)

Lontact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5377 8431
Fax: +46 (0)8 537 8335
Email: Peter Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.

Seq primer: M13 reverse primer.
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                                                                                                                            CN226782 744 bp mRNA linear EST 09-APR-2004 AJE004H01.abl RJtestis Gallus gallus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                        Gallus gallus
Waryvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Silva,C.S., Jorge,E.C., Patricio,M., Ledur,M.C. and Coutinho,L.L.
Discovery of new genes expressed in the chicken pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome_lib="RJtestis"
/note="Organ: testis, Vector: pSPORT-1; Site 1: Hind III
Site_2: EcoRl; The cDNA libraries were created with the
Superscript Plasmid System (Invitrogen)."
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 744)
Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and
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55.8%; Pred. No. 37;
tive 9; Mismatches

    . 744
    /organism="Gallus gallus"

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/sex="male"
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Gallus gallus
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526 CAACGAGATCAAGTTT 541
81 UAGCGACAGCAU 96
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Matches 29; Conservative
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/clone_lib="HTI"
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/note="Vector: pSPORTI; Site_I: NotI; Site_2: SalI; This
cDNA library was constructed with the SuperScript Plasmid
System with Gateway Tecnology kit (Invitrogen), following
manufacture's protocols. Plasmid DNA was purified using a
modified alkaline lygis method. Sequencing reactions were
conducted using the kit Big Dye Terminator Cycle
Sequencing Ready Reaction (Applied Biosystems) according
to the manufacturer's recommendations. Clones were
sequenced by the 5' end with T7 primer. Sequencing
reactions were analyzed on ABI Prism 3100 Genetic Analyzer
(Applied Biosystems). The quality and clustering of the
ESTE were analyzed using the softwares Phred/Cap3. Only
EST sequences with Phred quality greater than 20 and at
least 150 bp were considered for clustering."
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Laboratory of Animal Biotecnology, Dep. of Animal Production ESALQ - University of Sao Paulo
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Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4434
Fax: 55 19 3429 4285
Fax: 55 19 3429 4285
FCR PRINCESILVAGESBIQ.USD.br and llcoutingesBalq.usp.br
BACKWARD: T7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and hypothalamus"
                                                                                                                                                                                                                                                                                                                          /organism≕"Gallus gallus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue_type="pituitary a'
'dev_stage="21 days old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="GGEZHT1005A10"
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3637, Ap
17553, A
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162, App
12508, A
13211, A
13212, A
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798, App
11795, A
7049, Ap
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15499, A
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21723, A
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                                                               April 19, 2005, 13:28:09; Search time 130 Seconds (without alignments) 1258.674 Million cell updates/sec
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5.1.6
Compugen Ltd.
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US-09-410-464-1

US-09-270-767-6441

US-09-270-767-21723

US-09-949-016-17037

US-09-949-016-17037

US-09-949-016-17037

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US-09-949-016-17840

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US-09-949-016-13840
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 version 9
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 366
                                Sequence 3, Appli
Sequence 35958, A
Sequence 1916, Ap
Sequence 16492, A
Sequence 16493, A
Sequence 16494, A
                                                                                                         Sequence 1, Appli
Sequence 1, Appli
equence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT Strauss et al.
TITLE OF INVENTION: Ploral homeotic genes for manipulation of flowering in TITLE OF INVENTION: Polar and other plant species.
TITLE OF INVENTION: Polar and other plant species.
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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4695, Ap
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US-09-513-9990-3558
US-09-328-352-1916
US-09-949-016-16492
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US-09-949-016-16493
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US-08-975-762-42
US-09-295-028-42
US-09-106-582-42
US-09-159-469-42
US-09-693-542-42
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US-09-643-990A-1
US-09-706-228-12
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                                                                                                                                                                                                                                                                                                     Sequence 608, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09410464
Patent No. 6395892
                                                                                                         1830121
1830121
577
2775
3786
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                      57178
786431
246
960
47781
47781
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Best Local Similarity
Matches 35; Conserv
US-09-328-352-608/c
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41
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 CGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.4%; Score 27.4; DB 3; Length 3791; 41.6%; Pred. No. 5.7;
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DIAMOND, LISA E
APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
APPLICANT: SHARMA, AJAY
TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC ANIMALS
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                         E: BROWDY AND NEIMARK, P.L.L.C.
419 SEVENTH STREET, N.W., SUITE 300
  67 UUUAGCAUAUGCCUUAGCGACAGCAUCUG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/675,773B
FILING DATE: 03-JUL-1996
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: COOPER, IVER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17037, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            Sequence 3, Application US/08675773B Patent No. 6166288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COOPER, IVER P. REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | |||
564 CATGGGGACTTGATGCT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 CUUAGCGACAGCAAGCU 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3791 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-09-949-016-17037/c
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                                                                                                     RESULT 5
US-08-675-773B-3/c
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21723
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                      Sequence 6441, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
TITLE OF INVERTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
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                                                                                                   32; Indels
                                                          Query Match 29.8%; Score 29.8; DB 3; Best Local Similarity 33.3%; Pred. No. 0.77; Matches 27; Conservative 22; Mismatches 32;
ORGANISM: Populus balsamifera subsp. trichocarpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 ITTTAAAAGTCGCTGAACCAACCGAAGATTCTG 319
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35.5%; Pred. No. 2.7;
tive 19; Mismatches
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; Sequence 21723, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                        1253 TTATGATTTTTCTTAGATACA 1273
                                                                                                                                                                                                                              68 UNAGCAUAUGCCUUAGCGACA 88
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 33; Conserv
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US-09-270-767-6441
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  ; US-09-410-464-1
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SOFTWARE: Patent.pm
SEQ ID NO 26061
LENGTH: 415
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASEUSEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                               Length 260286;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESEQ for Windows Version 4.0
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; Sequence 12106, Application US/09949016
; Patent No. 6812339
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14382 AAATGCCCTAGGGGCAG 14366
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Best Local Similarity 39.0%
Matches 30, Conservative
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Best Local Similarity 39.0%
Matches 30; Conservative
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                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                     SEQ ID NO 17037
LENGTH: 260286
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LENGTH: 260293
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US-09-513-9999C-21500/c
; Sequence 21500, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

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US-09-513-999C-26061/C

| Sequence 26061, Application US/09513999C
| Sequence 26061, Application US/09513999C
| Patent No. 6783961
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclert, A.
| APPLICANT: Giordano, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| Patent No. 6783961
| FILE REFERENCE: 59.US2.REG
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT FILING DATE: 1090-02-24
| PRIOR APPLICATION NUMBER: US 60/122,487
| PRIOR APPLICATION NUMBER: US 60/122,487
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APPLICANT: Giordano, J.Y.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REPERBYCE: 59. US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-26
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
SOFTWARE: PATENT. B. SEG ID NOS: 36681
SEG ID NO 21500
LENGTH: 208
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Best Local Similarity 48.4%; Pred. No. 4.
Matches 30; Conservative 10; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%; Score 27; 39.8%; Pred. No.
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US-09-513-999C-21500
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Matches 33; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 340
OTHER INFORMATION: y=c o
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 344
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94639 AGGAAGGCTTTGATGCACAATTTCTCTCCAAAATCCATTCAAGTACCAAAAAGTTCTTCC. 94580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                              69 UAGCAUAUGCCUUAGCGACAGCAUCU 98
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Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus au
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141574 TGCAGAAAACTTAGCTGCAGCA 141595
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, Application US/08956171E Patent No. 6593114
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(150597)
; OTHER INFORMATION: n = A
US-09-949-016-15379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (1)...(15059
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                                                                                                                                                                                     US-09-949-016-15379
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ORGANISM: Human
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                                                                                                                             Sequence 3637, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT PELLACATION NUMBER: US/09/949,016

CURRENT PELLING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-09-08

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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46.3%; Pred. No. 23;
iive 9; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local Similarity 38.9%;
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Best Local Similarity 46.31
Matches 38; Conservative
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                 AG 208
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US-09-949-016-17553
                                                                                                                JS-09-949-016-3637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3637
LENGTH: 6944
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                      209
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Sequence 15379, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/231,498

FRIOR PELING DATE: 2000-10-03

FRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESQ for Windows Version 4.0

SEQ ID NO 15379

LENGTH: 150597
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                      Best Local Similarity 31.29
Matches 24; Conservative
                                                                                                         linear
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ORGANISM: Human
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                                                                                                         TOPOLOGY: 1
US-08-781-986A-162
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCUU 81
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 162: US-08-956-171E-162
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO: 162: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 CGCTTCTGCGATTTTCT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 AGCGACAGCAAGCUUCU 98
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 24; Conserva
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PROGRAMMENTS: 1876

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4 (bases 1 to 199415)
Han,J., Montgomer,Y.K.T., Grills,G., Chiu,D., Decker,J., Fusina,M., Goltz,J., Haider,Y.K.T., Grills,G., Chiu,D., Decker,J., Fusina,M., Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.
Direct Submission
Submitted (05-SEP-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA 02139, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUL-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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AC110847 Rattus no
AC10165 Rattus no
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AC10697 Rattus no
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AC129014 Rattus no
AC129018 Rattus no
AC12901 Rattus no
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AF522912 Tachyglos
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AF522916 Tachyglos
AF522916 Tachyglos
AF318058 Sequence
AC137289 Rattus no
AC137289 Rattus no
AC137280 Rattus no
                                                                                     April 19, 2005, 13:28:09; Search time 1693 Seconds (without alignments) 2862.092 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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CQ451733
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AE017283
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AR318058
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AC114165
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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30.4 366
30.4 3185
30.4 46077
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30.4 207260
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Perfect score:
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C 21 22 23 C 24 C 24 C 24 C 25 C 26 29 29 30 C 31 C 31 C 31 C 31 AC084053 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE AUTHORS	шшшшшшш аааааааааааааааа	0000000	1.4 30.4 21303. 1.4 30.4 218153. 1.4 30.4 218153. 1.2 30.2 22952. 1.2 30.2 22952. 1.2 30.2 22952. 1.3 30.2 22952. 1.3 30.2 22952. 1.3 30.2 24075. 1.4 30.4 21815. 1.5 30.2 22952. 1.6 29.8 21213. 1.8 29.8 20224. 1.8 29.8 20224. 1.8 29.8 20224. 1.8 29.8 2124. 1.9 2.8 2234. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.9 2.8 2124. 1.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	252953333333333333333333333333333333333	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		31482 33588 31046 31256 3109311 33102 33102 33102 55708 33102 57708 5770	d g g g g g g g g g g g g g g g g g g g	DNA lin OBOME 3 BAC, iata; Verteb rognathi; Mu , Chiu,D., D ikhes,I.P., Kucherlapati , Chiu,D., D ikhes,I.P.,	+C 0 5 u.s.	- ביס או ש	AC131482 Rg AC139588 Rg AC139588 Rg AC139588 Rg AC109911 Rg AC109911 Rg AC109911 Rg AC109911 Rg AC109911 Rg AC10961 Pg AC	AC131482 Rattus AC13958 Rattus AC112576 Rattus AC112576 Rattus AC139211 Rattus AC139312 Mus mus AC139312 Mus mus AC145887 Pan ti AC145887 Pan	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	nno nno nno nno nno nno nno nno nno nno
JOURNAL	TCE TATE	Subm Eine Bron 3 (Submitted Submitted Einstein (Bronx, NY 3 (bases	K 1001	2-0CT lege 461, to 19	of of USA 941	_ ; <u>;</u>	، وب	tment of Genome Cer	of Molecul Center, 1	cula,	lar Geneti 1300 Morri	Genetic Morris	cs, l s Par	, Albert Park Ave	
AUTHORS)RS	Han, J., Goltz, J Perera, Direct	an,J., M oltz,J., erera,A. irect Su	Mont Ha	<pre>Han,J., Montgomery,K.T Goltz,J., Haider,A., Hi Perera,A., Shim,C., Tho Direct Submission</pre>	Α. Υ.Κ.	1,4 Cma	Ξ,.	s,G., Chiu,D., Dec) Ioshikhes,I.P., Lee and Kucherlapati,R	iu, D s, I.l erlaj	P. D	Decker,J. , Lee,B., ti,R.		, Fusir Long, J.	Fusina,M., ng,J.,	Σ.

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STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences (A. Smit and P. Green, Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity matches are annotated as similar.
                                                                                                                                                                                                                              CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCING READ COVERAGE: Attempts are made to complete double strandedesquence for all regions. All sequence is completed to a stranded sequence for all regions of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the amnotation asthow Coverage. Low coverage in the annotation asthow Coverage. Low coverage inhappes are verified by PCR product size verification or verification of forward and reverse reads from clones which span
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.
On Sep 5, 2002 this sequence version replaced gi:22002115.
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                                                                                           Center Code: HPGC
Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu

    Distribution of Quality < 40 Bases:</li>

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Fraction of Phrap value < 40: 0.000326
Error Rate in Consed: 0.00 per 10,000 bases
Number of N's in consensus: 0
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Phrap Value Range
                                                            Harvard Partners Genome Center
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Chemistry: Dye-terminator Big Dye; 100$
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Center project name: ADW
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/chromosome="3"
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complement (557. .1289)
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COMMENT
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/ryt family="CT-rich"
complement (15461. 15814)
/rpt family="MJT2B3"
complement (15861. 15915)
/rpt family="MJT2B3"
complement (15831. 15915)
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rpt_family="(CAAA)n"
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complement(20510. .22297)
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22298. .23888
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ement (720)
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064. .927c
                                   /rpt_family="AT_rich"
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                                                                         complement (1888. .3694)
                                                                                                                                                                          complement (5123. .5507)
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complement (5512. .6982)
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8325. .18841
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                                                                                                                        252. .444i
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/rpt_family="LlMA7"
|304. .131
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omplement(13902. .
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10957. .10067
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696. .4251
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                  The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                        This sequence is the entire insert of the clone. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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/rpt_family="MalR"
6071. .616?
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/clone_lib="RPCI-23"
171. 557
/rpt_family="MalR"
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1200. .12140
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7137. .7220
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1887. .2101
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2792 . 2918
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2916 . 3397
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.0673. .11051
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12715. 12907
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12908...13742
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2674. .12714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="8"
                                                                                                                            http://genome.wustl.edu
                                             MAPPING INFORMATION:
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Submitted (05-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 05-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 201197)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base 1 to 20197)

Trani,L. and Cotton,M.

The sequence of Mus musculus BAC clone RP23-433F5
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        AC125279 201197 bp DNA linear ROD 05-N
Mus musculus BAC clone RP23-433F5 from 8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   37 CGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCUUAGCGACAG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                               Length 199415;
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                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                 DB 10;
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                               ; Score 32.2; DE; Pred. No. 8.6; 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: M_BA0433F05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- Genome Center
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2 (bases 1 to 201197)
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25210.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS JOURNAL

COMMENT

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TITLE

RESULT 2 AC125279/c LOCUS DEFINITION

Matches

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Length 201197;

Indels

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Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Ruzny, D. Marie., Matzker, M. Lee., Abramazon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Badan, H.,

Baldwin, D., Bandaranatke, D., Barber, M., Barnstead, M., Benahmed, F.,

Baldwin, D., Bandaranatke, D., Burrell, K., Calderon, E.,

Cardensa, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Dr. Cozdenson, C., Corkell, R., Cox, C., Coyle, M., Center, A., Dr. Cozdenson, C., Coyle, M., Cree, A., D., Souza, L.,

Davila, M.L., Davis, C., Deramo, C., Ding, Y., Dunh, H., Duya, K.,

Davaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Becotto, M., Elagg, N., Forbes, L., Falls, T., Fan, G.,

Praser, C., M., Gablish, A., Ganter, M., Genera, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevra, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Henderson, N., Hernandez, M., Handl, C., Hamilton, C., Hamilton, K., Harvey, X., Havla, K., P., Hada, M., Handl, S., Howels, D., Jackson, A., Jackson, L., Johnson, R., Mandandan, D., Lui, W., Man, J., Kan, Y., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mandiadren, B., Mandiadren, M., Martin, R., Mandiadren, M., Mandiadren, M., Mander, M., Ben, Y., Reufer, A., Popez, R., Reilly, M., Ren, Y., Reufer, M., Ren, Y., Reufer, M., Ren, Y., Reufer, M., Ren, Y., Reufer, M., Ren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus clone CH230-42M10, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                       2984 GCAGGCTTTCATCCCAGCATCTGATTCTTGATGATAAATCTAACAATTGAG 2925
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus (Norway rat)
                                                                                                                                                                DB 10;
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                                                                                                                                                              31.2%; Score 31.2; D 32.6%; Pred. No. 19; ive 24; Mismatches
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Matches 30; Conservative
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AC110847
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:=-11.21)"
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17836. 18263
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omplement(26924.
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4784.
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230<u>8</u>.
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us-09-529-397c-25.rge

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La Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23321762.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the setimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svarek, A., Tabor, P., Taylor, P., Taylor, P., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Walson, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Walten, R., While, F., Willson, R., Wlersty, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, Y., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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170421: contig of 1410 bp in length
170521: gap of unknown length
172029: contig of 1508 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 187606)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 187606)
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                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
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31268
77384
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169012
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170522
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AUTHORS
TITLE
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AC103165 221991 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-194N19, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGAGUGGAGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCAUCAAACCAGUUAUAAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC103165.6 GI:30578614
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%; Score 30.8; DB 2; Length 187606; 34.7%; Pred. No. 26; ive 22; Mismatches 42; Indels 0;
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'n length
                                     length
bp in length
                                                                        length
bp in length
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                                                                                                                                                                                                                                                             length
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length
                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
                                                                                                                                                                contig of 1342 b
gap of unknown 1
contig of 1543 b
                                                                          unknown
of 1562
                                                                                                                               contig of 2122
                                                                                                                                                                                                                                             184491: contig of 2318
                                                                                                                                                                                                                                                             184591: gap of unknown
187606: contig of 3015
                                     unknown
                                                        of 1297
                                                                                                               unknown
                                                                                                                                                   unknown
                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA/db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                clone="CH230-42M10"
                                                      contig c
gap of c
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                   contig
gap of
                                                                                                               gap of
                                                                                                                                                                                                                         182173: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_contig"
95087. .96968
                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="wgs_contig"
18318. .29829
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77484. .79244
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[31603. .132754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="wgs_contig"
45131. .150091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="wgs_contig"
67411. .168911
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Best Local Similarity 34.7%
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:25087265.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Dinny, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Durnin, K., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Edgen, C., Evans, C.A., Falls, T., Falls, T., Falls, M., Prages, K., Garcia, A., Garrar, M., Gabreis, A., Ganta, R., Garcia, A., Garrar, M., Gabreis, R., Haalland, M., Hamill, C., Hamilton, C., Hamilton, K., Harnandez, R., Hines, S., Hawes, A., Henderson, N., Hernandez, M., Guevara, W., Gubergerorgis, R., Halaland, M., Hamill, C., Hamilton, K., Hollins, B., Howells, S., Hluyk, S., Hume, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hluyk, S., Hume, J., Idlebird, D., Jackson, A., Karpath, S., Kelly, M., Martinez, B., Mandenhari, M., Martiney, S., Molcedd, M., Morris, K., Morris, S., Munidas, M., Norris, S., Dun, H., Pull, H., Kelly, M., Renz, M., Rese, R., Reigh, R., Reere, K., Regier, M.A., Reigh, R., Kelly, M., Strong, R., Reves, C., Primus, E., Pull, H., Perez, A., Perez, L., Frankoch, C., Shafish, S., Sherty, G., Shartsher, M., Savery, G., Scherer, S., Soretle, R., Ware, M., Sodergren, R., Sone, Y., Yalles, M., Strong, R., Warren, R., Wall, M., Strong, R., Warren, R., Wall, M., Yer, Shart, R., Warren, R., Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
Direct Submission
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC114165 231814 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-165814, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alah, D. Marie., Metzker, M. Lee., Amin, A., Anguiano, D., Anlah, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carter, K., Cavacron, E., Cardenas, V., Carter, K., Cavacs, I., Censar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
                                                     Assembly program: Atlas 3.0;
Consensus quality: 210155 bases at least Q40
Consensus quality: 214132 bases at least Q30
Consensus quality: 121411 bases at least Q30
Estimated insert size: 222472; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 UAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUUAGCAUAUGCCUUAGCG
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Rattus no_vegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
Center clone name: CH230-194N19
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/note="wgs end_extension
clone_end:5p6"
39959_.40695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA'
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BH339559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39959. .40695
/note="clone_boundary
clone_end:Sp6
site:EcoRI
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AC114165.4 GI:30579575
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AC114165/c
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VERSION
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Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from

Consensus quality: 219004 bases at least Q40 Consensus quality: 222024 bases at least Q30 Consensus quality: 224099 bases at least Q20 Estimated insert size: 229718; sum-of-contigs estimation

Center clone name: CH230-165B14 Center project Information

.-- Summary Statistics

Assembly program: Atlas 3.0

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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., De Auda, C., Denderich, D., Degado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Degado, C., Engley, M., Falagy, M., Farago, F., Fang, C., Farago, F., Fang, C., Farandez, S., Finley, M., Flagg, N., Forbes, L., Footer, M., Gebregocrgis, E., Geark, K., Garla, R., Garcia, A., Garner, M., Gebregocrgis, E., Geark, K., Gill, R., Graddy, M., Guerra, W., Guevara, M., Gebregocrgis, E., Geark, K., Gill, R., Graddy, M., Guerra, W., Guevara, M., Harrandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hlayk, S., Klan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Molivet, A., Karpathy, S., Kelly, S., Khan, T., Mangom, B., Mapue, P., Martin, R., Martin, R., Martin, R., Martin, M., Mahmolu, M., Malloy, K., Mangum, A., Mapue, P., Martin, R., Mangum, A., Morgan, P., Morgan, M., Morgan, R., Morgan, R., Morgan, M., Morris, S., Munidas, M., Murphy, M., Martin, R., Mall, M., Parez, A., Petera, L., Fander, R., Sedergren, B., Sadergren, B., Sadergren, B., Sadergren, B., Sadergren, R., Street, A., Street, M., Strong, R., Villasan, R., Wille, R., Willson
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using ALIas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs-scaffold'). Within each contigs caffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Genome Sequencing Consortium.
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JOURNAL
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Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

COMMENT

Contact: hgsc-help@bcm.tmc.edu

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 231814: contig of 231814 bp in length.
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Rattus norvegicus clone CH230-43H7, *** SEQUENCING IN PROGRESS ***.
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/organism="Rattus norvegicus"
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clone_end:T7"
                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db xref="taxon:10116"
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93963. .96094
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228398. .231814
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clone_end:Sp6
site:EcoR1
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119152. 121641
/note="wgs_contig"
complement(227278. .
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REFERENCE AUTHORS

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Memmalias Entherias, Rodentias Sciurognathi, Mutidae; Muzinae;

Memmalias Entherias, Rodentias Sciurognathi, Mutidae; Muzinae;

Memmalias, Defined as Recommendation of the control of the
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AUTHORS TITLE JOURNAL

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AUTHORS TITLE JOURNAL

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bom.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a "working draft" sequence. It currently

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* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

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by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-seaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 212738 bases at least Q40
Consensus quality: 215401 bases at least Q30
Consensus quality: 217067 bases at least Q20
Estimated insert size: 219523; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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/note="wgs end_extension
clone_end:T7"
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clone_end:T7"
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/db_xref="taxon:10116"
/clone="CH230-43H7"
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85851. .88514
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/note="clone_boundary
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site:EcoRI
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site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                Narany, Danaie, Mezker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allan, L., Allan, H., Albarbooks, S., Amin, A., Aggudano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balabrooks, S., Amin, A., Aggudano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baladrin, D., Bendaranike, D., Barbare, M., Barnstead, Benahmed, F., Biswalo, K., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cradenas, V., Carter, C., Cavazo, I., Ceasar, H., Center, A., Clacko, J., Chavazo, L., Char, E., Char, C., Coyle, M., Cree, D., D'Gouza, L., Davila, M., Cree, M., Dinyal, E., Bares, C., Dayay, Carroll, L., De Anda, C., Dederich, D., Denson, S., Derson, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Ebere, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Eberson, C., Ding, Y., Chan, C., Falls, T., Fand, G., Ferrandez, S., Finly, M., Flaggi, N., Guevar, M., Genze, P., Ferrandez, S., Finly, M., Guerra, M., Gavaza, M., Genzeorgis, E., Geer, K., Gills, M., Guerra, M., Gavaza, M., Herrandez, S., Finly, M., Filogy, M., Guerra, M., Gavaza, M., Herrandez, S., Finly, M., Filogy, M., Guerra, M., Gavaza, M., Herrandez, R., Haviak, P., Haviak, P., Hander, D., Idahing, B., Montandez, R., Haviak, P., Haviak, P., Hander, B., Johnson, R., Johnson, J., Jang, H., Johnson, B., Johnson, R., Marja, M., Manda, M., Mayam, A., Mayam, A., Mayam, P., Martin, K., Martin, 
                                                         AC099144 238172 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-68F7, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 238172)
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                       HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium,
                                                                                                                                              AC099144.5 GI:30522119
                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 238172)
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RESULT 7
AC099144/c
                                                   LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                 ORGANISM
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AUTHORS
TITLE
JOURNAL
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23264509. The sequence in this sequence version replaced gi:23264509. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold') Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estimated insert size: 230633; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 GCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCU 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                         shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Atlas 3.0;
Consensus quality: 220106 bases at least Q40
Consensus quality: 222963 bases at least Q30
Consensus quality: 224727 bases at least Q20
Estimated insert size: 230633; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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Best Local Similarity 43.1%; Pred. No. 26;
Matches 25; Conservative 16; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-68F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: CH230-68F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1721
/note="wgs_end_extension
clone end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end_sequence:BH351992"
234541. .234906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BH351956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234541. .234906
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8345. . . 8845
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: GGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236172. .238172
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site:EcoRI
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AC129051/c LOCUS DEFINITION

RESULT 8

셤

ACCESSION

VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS

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* NOTE: Estimated insert size may differ from sequence length

* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: CH220-8977

Assembly program: Prag; CH220-8977

Consensus quality: 217247 bases at least Q40

Consensus quality: 2222917 bases at least Q30

Consensus quality: 226268 bases at least Q30

Consensus size: 225713; aum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 247784: contig of 247784 bp in length
247785 247864: gap of unknown length
247875 249178: contig of 1294 bp in length
249279 249278: gap of unknown length
249279 250740: contig of 1462 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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clone="CH230-89P7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="clone boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GQOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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/note="wgs_contig"
39370. .40<u>8</u>12
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164963. 166515
/note="wgs_contig"
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                                                                  REFERENCE
AUTHORS
                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                          TITLE
                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   To Dasses 1 to 250740

In Dasses 1 to 250740

Anyalebechi, V., Angleri, M., Beca, E., Baden, H.,

Anyalebechi, V., Anyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldrin, D., Bandaranalke, D., Barber, M., Barastead, M., Benahmed, F.,

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Bishdin, D., Bandaranalke, D., Barber, M., Barastead, M., Benahmed, F.,

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Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Deederich, D.,

Davila, M., L., Dugan-Rocha, S., Dum, A., Durbin, K., Duval, B., Eaves, K.,

Band, A., Becotto, M., Eugene, C., Ding, Y., Dinh, H., Poster, P.,

Rernandez, S., Filly, M., Flaggy, N., Forbes, L., Foster, M.,

Gebregeorgis, E., Geer, K., Gill, R., Handerson, N., Hennandez, J.,

Hernandez, R., Haviak, P., Hawes, A., Handerson, N., Hennandez, J.,

Hernandez, R., Haviak, P., Hawes, A., Handerson, N., Hennandez, J.,

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Markowy, Y., Marchis, S., Maldun, S.L., Moyer, S.,

Mandgun, L., Jacob, L., Janag, H., Wantin, K., Martin, K., Martin, K.,

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Margon, R., Savery, G., Nauron, M., Robers, R., Reigher, M., Reigher, R.,

Shetty, A., Shetty, A., Siecon, I., Sitter, C. D., Smajs, D.,

Shetty, S., Shetty, A., Siecon, I., Shetter, S., Shett, R., Band, M.,

Mangun, B., Savery, G., Song, X., R., Song, Y., Pale, S., Bang, J.,

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Mang, S., Warsen, M., Walse, R., So
        129774 GCATATTTCGATTCCTTCTTGCCTTAAACCAATTTGAACGTGGTCTTACAAAATCTCT 129717
                                                                                                                                                                              AC129051 250740 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-89P7, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                          AC129051.3 GI.25139158
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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Query Match
Best Local Similarity 46.8%
Matches 36; Conservative
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AE017283_17
AE017283_18
AE017283_19
AE017283_20
AE017283_21
AE017283_23
AE017283_23
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AE017283_07
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AE017283 15
WPCOMMENT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                      23 GCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCU 80
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                                                                                             Gaps
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                                                                DB 2; Length 250740;
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Human polynucleotides and polypeptides encoded thereby
Patent: WO 0195523-A 17493 06-DEC-2001;
Curagen Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 748;
                                                              30.8%; Score 30.8; DB 2; Length 2 43.1%; Pred. No. 27; Live 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Indels
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/organism="bropionibacterium acnes"
/mol_type="unassigned DNA"
/db_xref="taxon:1747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                               CQ451733 748 bp DNA Sequence 17493 from Patent WO0192523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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CORIXA CORPORATION (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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46.8%; Pred. No. 20;
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Sequence 78 from Patent WO0181581.
CQ363795.1 GI:41300489
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/note="wgs_contig"
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Propionibacterium acnes
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CCCTGGGCACGGGAAGC 241
                                                                                                                                                                                                                                                                           CQ451733.1 GI:41420097
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                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 CCUUAGCGACAGCAAGC
                                                              Query Match 30.8%
Best Local Similarity 43.1%
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
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      misc feature
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CQ363795
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Continuation (16 of 26) of AE017283 from base 1500001. (AE017283 Propionibacterium acnes P
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Tachyglossus aculeatus clone TaG7 type I interferon gene, partial
                                                                        18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG 77
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Tachyglossus aculeatus
Eukaryota, Metzacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Tachyglossidae; Tachyglossus.
                                      Gaps
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Length 15776;
                                      Indels
                                    29;
30.6%; Score 30.6; DB 6;
46.8%; Pred. No. 25;
tive 12; Mismatches 29;
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310000
410000
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710000
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AF522912.1 GI:27451581
                                                                                                                                                                                                                                                                                                Sequence split into 26 fragments
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1300001
1400001
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300001
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900001
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2500001
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/product="type I interferon"
/protein id="AAO14988.1"
/db_xref="GI:27451586"
/translation="NI FSRHRSQTGWDEAIVEKFLHGVHQEMVWLELFLEEEMGWENS
TLRRDISLHIKSYFKRWMDYLKGRNYSS"
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TLRRDISLHIKSXFKRMMDYLKGRNYSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Monotremata, Tachyglossidae, Tachyglossus.

    (bases 1 to 217)
    (barrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and

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Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Tachyglossus aculeatus clone TaG31 type I interferon gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-J7N-2002) School of Science, Food and Horticulture,
University of Western Sydney, Locked Bag 1797, Penrith South DC,
NSW 1797, Australia
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Tachyglossus aculeatus
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/organism="Tachyglossus aculeatus"
/mol_type="genomic DNA"
/db_xref="taxon:9261"
/clone="Tad31"
                                                                   aculeatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 30.4%; Score 30.4; DB 4; Similarity 41.7%; Pred. No. 21; 30; Conservative 16; Mismatches 26;
                                                                                                                                                                                                             /product="type I interferon"
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:1. .>217
                                                             /organism="Tachyglossus
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      Location/Qualifiers
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/codon_start=2
                                                                                                                                                      /clone="TaG11"
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AF522916.1 GI:27451589
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Best Local Similarity
Matches 30; Conserva
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AF522916/c
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                                                                                                                                                                                                                               2 (bases 1 to 217)
Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi,
Bukamalia, Monotremata, Tachyglossidae; Tachyglossus.

1 (bases 1 to 217)
Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
                                                       A survey of type I interferons from a marsupial and monotreme: implications for the evolution of the type I interferon gene family
   Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="NIFSRNHSQTGWDEAIVEKFLHGVHQEMVWLGLFLEEEMGWENSTLRRDISLHIKSYFKRMMDYLKGRNYSS"
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Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Tachyglossus aculeatus clone TaG11 type I interferon gene, partial
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Submitted (19-JUN-2002) School of Science, Food and Horticulture,
University of Western Sydney, Locked Bag 1797, Penrith South DC,
NSW 1797, Australia
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protein_id="AAO14986.1"
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Breton,G. and Bush,D.
Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics
Patent: US 6562958-A 608 13-MAY-2003;
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